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Instructions to authors

Scope of the journal

Nucleic Acids Research provides rapid publication for papers on physical, chemical, biochemical and biological aspects of nucleic acids and their constituents.

Organization of the journal

The Contents Page lists papers under the headings: Surveys and Summaries, Molecular Biology, Enzymology, Chemistry, For The Record and RFLP Reports. Authors are asked to indicate the heading under which they would expect their paper to appear.

Papers (including figures and tables) must not exceed 20 pages in length. Restriction maps and nucleic acid sequences which have been determined by established methods should be presented in the briefest possible fashion. Data that support the conclusions are generally not published but must be available for the referees.

Criteria for acceptance

The journal can publish only a fraction of the manuscripts it receives. For this reason, the Editors insist that all manuscripts considered for publication meet the criteria of originality, timeliness, significance and scientific excellence. Because technical progress in the isolation and sequence analysis of both RNA and DNA has greatly increased the amount of new sequence information, the Editors favour those manuscripts in which new sequences are accompanied by complementary data bearing on genomic organization, transcription, RNA processing, expression and genetic analysis. Nucleic Acids Research cannot serve as a mere repository for nucleic acid sequence information; the reported sequence must shed significant new light on basic questions of structural or functional interest. Sequences of cDNAs or genes whose gene products are not relevant to nucleic acids are not acceptable as full length papers. The Editors encourage those sequence manuscripts in which the gene product interacts with nucleic acids, as well as those in which information of special interest to the nucleic acid field emerges: e.g., those dealing with gene regulation or unusual gene organization. They also consider for inclusion manuscripts dealing with comparative sequence analyses if the genes under study are of relevance to nucleic acid metabolism. Sequences of genes for well studied RNAs (as well as the RNA sequences themselves) are not acceptable unless of unusual interest. However, all sequence papers are considered for publication in the 'For The Record' format. 'Methods papers' are considered only if an outstanding and potentially very useful advance is clearly documented. Otherwise, we prefer that such information be included in the Methods section of a paper presenting new data of interest. Except in extraordinary cases, manuscripts presenting construction of cloning vehicles or clone banks, preparation of monoclonal antibodies, identification of isoschizomer restriction enzymes

or those describing routine synthesis of oligonucleotides are not published.

Chromosome assignment papers where only cytological data are presented are not acceptable. Likewise, simple NMR assignment papers are not acceptable. Only those which present new information not previously available from other methods are considered. Manuscripts dealing with small molecule-nucleic acid interactions are considered only if they present substantial new information relevant to nucleic acid structure. Clones, strains or programs described in *Nucleic Acids Research* should be made available. Papers dealing with computer analysis of already published sequences are acceptable only if new and interesting findings emerge.

Surveys and Summaries

These are intended to provide a format for brief reviews which collect information not previously available in a single article.

For The Record

In some cases, manuscripts not suitable for inclusion as regular papers may be considered in this section. See detailed instructions in Volume 15 number 1, January 12, 1987.

Restriction Fragment Length Polymorphisms (RFLPs)

See detailed instructions in Volume 15 number 1, January 12, 1987.

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All computer manuscripts should be sent to: The Editor, *Nucleic Acids Research*, IRL Press Inc, PO Box Q, McLean, VA 22101, USA.

All manuscripts on chromatin structure should be submitted directly to:

Dr S.C.R.Elgin, Department of Biology, Washington University, Campus Box 1137, St. Louis, MO 63130, USA. If a manuscript is rejected, normally only the original copy, together with all the figures, are returned to the author.

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